Supplementary data

Table S1: Clinical characteristics from 38 patients diagnosed with T-cell ALL in Sweden, 1998-2006

Characteristics	Number of patients (total n = 38)
Gender	
Female	6
Male	32
Age at diagnosis (years)	
1-5	12
>5-10	15
>10-17	11
Leukocytes at diagnosis (x10^9/L)	
<50	2
≥50-100	4
>100	18
Missing data	14
Hematopoietic stem cell transplantation	
Yes	19
No	19
Relapse	
Yes	11
No	27
Overall survival ≥ 5 years	
Yes	28
No	10

Table S2: Karyotype for the studied patients diagnosed with T-ALL between 1998 and 2006.

No.	Gender	Age at diagnosis (years)	Karyotype
1	Male	10	46,XY[6]
2	Female	8	46,XX,t(6;11)(q26-27;q23),der(12)t(12;17)(p11.2;q23)
3	Male	13	46,XY
4	Male	2	46,XY[25]
5	Male	12	46,XY,?t(2;10)(p2?;p?)[4]/46,idem,t(2;9)(p1?;p?)[5]/46,XY[3]
6	Male	12	46,XY
7	Female	3	46,XX pb
8	Male	4	46,XY,add(9)(p13)[29]/46,XY[20]
9	Male	9	46,XY,add(3)(p13)[13]/46,XY[1]

10	Female	13	46,XX[16]
11	Male	2	46,XY[17]
12	Male	9	46,XY[20]
13	Male	9	47,XY,i(9)(q10),t(10;11)(p13;q14),+der(19)[13]/46,XY[15]
14	Female	13	46,XX[11]
15	Male	11	46,XY[21]
16	Male	9	44-46,XY,add(2)(p23),t(11;14)(p13;q11)[14]/46,XY[16]
17	Male	7	.ish.??,X?,del(9)(p21p21)x2
18	Male	6	45-46,XY,add(1)(p36),-5,t(8;14)(q24;q11),i(9)(q10),-16,+2mar[cp23]/46,XY[1]
19	Male	4	45,XY,-1,-3,-3,-4,-5,-6,-8,-10,del(11q),-12,-12,-15,mar,inc[cp21]/46,XY[1]
20	Male	4	47,XY,del(6)(q23),+8[9]/46,XY[16]
21	Male	8	46,XY,del(5)(q?),der(14)ins(14;5)(q11;q?q?).nucish.del(9)(p21p21)
22	Male	2	46,XY[21].ish.del(9)(p21p21)[79%]
23	Male	5	46,XY,t(7;9)(q3?4;q3?2)[10].ish.del(9)(p21p21)x2,der(11)t(7;11)(q3?4;p1?3)/46,XY[15]
24	Male	3	45,XY,dic(9;20)(p13;q11)[3]/46,XY[21]
25	Male	10	46,XY,der(9)t(7;9)(q21;p13)[22]/46,XY[8]
26	Male	14	47,XY,+der(6)t(6;7)(q12;q31),t(11;19)(q23;p13)
27	Male	10	46,XY[21] pb
28	Male	1	47,XY,+10,add(11)(q23).ish.der(11)(q23)/46,XY
29	Male	3	46,XY[25]
30	Female	14	Missing data
31	Male	17	Missing data
32	Male	8	Missing data
33	Male	9	47,XY,+9[7]/46,XY[16]
34	Male	7	46,XY,inv(9)(p11q13)c
35	Male	13	46,XY[24]
36	Male	9	46,XY,+mar,inc[2]/46,XY[25].ish.del(9)(p21p21)
37	Male	14	45,XY-9,inc
38	Female	2	46,XX,t(11;20)(q23;q?)[21]/46,XX[8]

Primer sequences used for *STIL-TAL1* analysis:

First reactions: *STIL* 5´AAGGGGAGCTAGTGGGAGAAA 3´, *TAL1* I 5´AGAGCCTGTCGCCAAGAA 3´ and *TAL1* II 5´TTGTAAAATGGGGAGATAATGTCGAC 3´

Second nested reactions: *STIL* 5´AAATTAAGCAGTGAAATCCT 3´, *TAL1* I 5´GAAGACCACATTAGAAGCA 3´ and *TAL1* II 5´CGACGTCACAAAGTTATGAGAACTAA 3´

Primer sequences for *NRAS* gene, used as integrity control.

Forward 5´ CTGGTGTGAAATGACTGAGT 3´

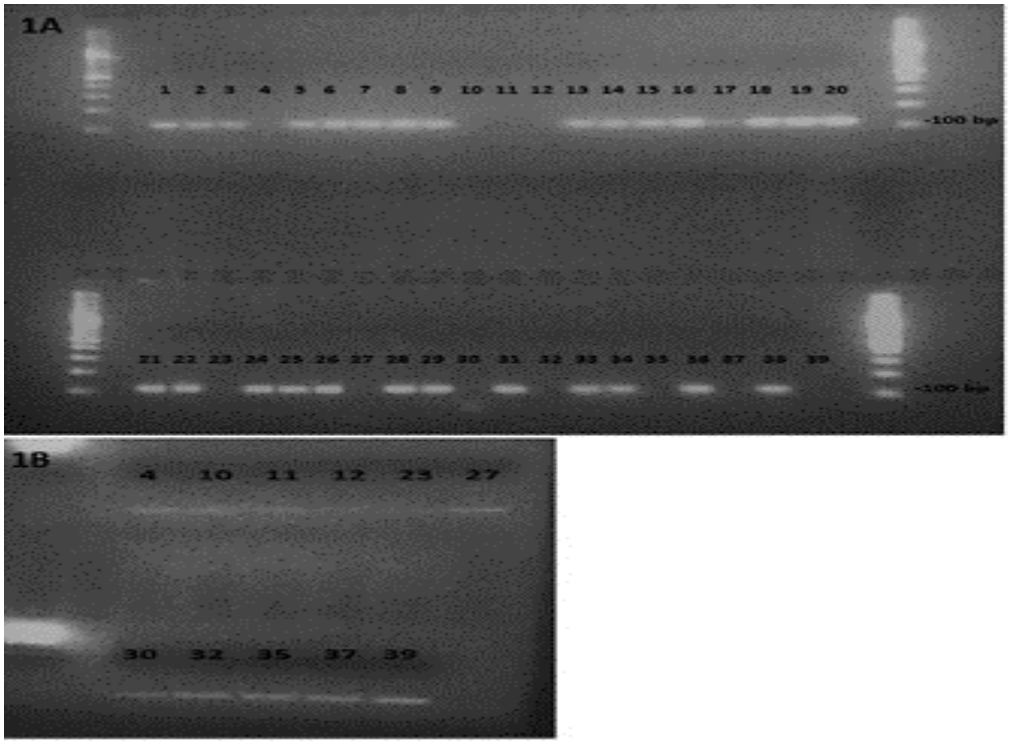
Reverse 5´GGTGGGATCATATTCATCTA 3´

***NRAS* integrity controls:**

Figure S1: NRAS control NBS.

A: WGA using 2.5µl NBS DNA. 28 positive samples and 11 negative samples after two sets of PCRs, using 2µl of WGA NBS DNA in first PCR and 2µl of first PCR reaction in second PCR.

B: New WGA for 11 previous negative samples using 5µl NBS DNA. 11 positive samples using 2µl of WGA NBS DNA in one set of PCR.



*Sample number 30 was later excluded from the study due to lack of clinical data.

Sensitivity assay for detection of *STIL-TAL1* type I deletions.

Serial dilutions of a DNA positive for *STIL-TAL* deletion were made from 10ng to 1pg each into 40ng DNA isolated from a patient with AML. Detection sensitivity of primers for C1 is this nested PCR assay was around 1 positive cell in 7000 cells.

Figure S2: DNA sequence of *STIL-TAL* deletions identified in two type I rearranged positive control DNAs.

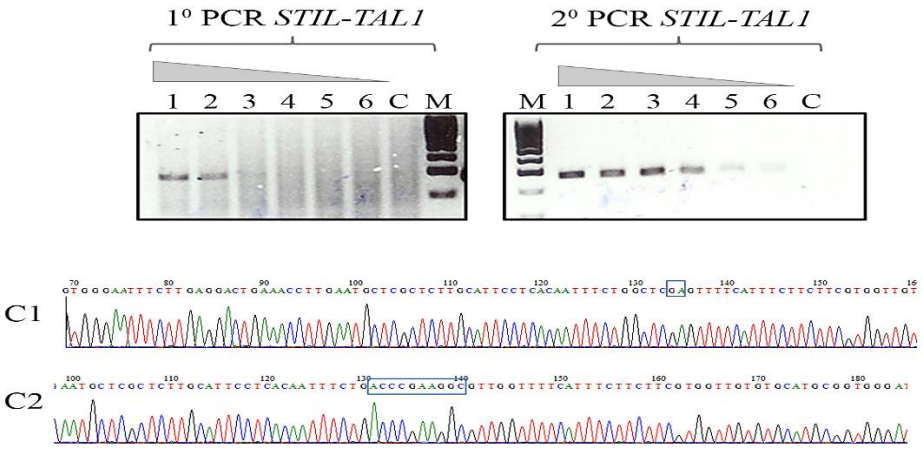


Figure S3: Nested PCR of Swedish T-ALL cases showing an absence of *STIL-TAL1* type II deletion.